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EXAMINER	
ZHAO, YU	

ART UNIT	PAPER NUMBER
2169	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/585,842	COX, ANTHONY	
	Examiner	Art Unit	
	YU ZHAO	2169	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *26 March 2009*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *25, 29-57* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *25, 29-57* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Response to Amendment

1. Acknowledgment is made of applicant's amendment filed on **March 26, 2009**.

Claims 25, 29-57 are presented for examination.

Claims 1-24 were cancelled per applicant's request**.**

Claims 26, 27, 28 are cancelled.

Claims 25, 29, 36, 44, 46 and 56 are amended.

Claim 57 is added.

Claim Objections is withdrawn in light of amendment by the applicant.

Response to Argument

2. Applicant's arguments filed in the amendment filed on **March 26, 2009**, have been considered but are moot in view of the new ground(s) of rejection.

Applicants argue that, "Importantly, all of the foregoing steps are performed in serial fashion, and this serial aspect of the present method and system is one of the distinguishing features of the invention that is nowhere found in either Califano or Bjornson et al., or in any of the references cited and applied herein."

The Examiner respectfully disagrees. The part that applicants argue, "All of the foregoing steps are performed in serial fashion," is not explicitly recited in the claim language. Further, Califano has showed the sequence matching is performed in the serial or sequence in Fig. 1A and 1B.

Applicants argue that, "As stated above, the present method proceeds in at least two phases in serial and this mode of operation confers clear advantages: the first groups of segments are compared before the second group is compared, as the results of that first comparison allow a more efficient second group comparison. Accordingly, as Bjomson describes a method of analysis of segments that proceeds in parallel, rather than in serial, and as there is no suggestion in Bjornson et al. of the present method, Bjornson et al. fail to cure the deficiencies of the primary reference to Califano, including those acknowledged by the examiner to exist, so that the combination of Califano and Bjornson in rejection of the claims particularly as presently amended, is untenable. Therefore, withdrawal of this ground of rejection is believed to be in order, and is requested."

The Examiner respectfully disagrees. Califano discloses "The BLAST technique **does an in-depth comparison** of the original and reference sequence **only if they satisfy an initial minimal similarity test** which can be performed very quickly. This is done by heuristically determining whether the length of the MSP (maximal segment pair) is above **a given threshold.** The MSP is

the pair of identical length substrings of the reference string and sequence string that has the best score for mutations. If this test is successful a more complete and costly similarity analysis is performed using FASTP-FASTA type algorithms. This reduces the amount of computation at risk of missing some matches that do not satisfy the initial criteria. About 20% of the similarities detected with the Needleman-Wunch algorithm are not picked up by BLAST. Also the approach remains inherently sequential since some computation must be performed for each token in the set of original strings."(Califano: column 2, lines 1-16) which indicate that there is a quick test try to find the pair of identical length substrings of the reference string and sequence string that ahs the best score. if it doesn't find it, it will not further continue the in-dept' comparison. Although, the term "group" is not used, the meaning of "group" is in the above cited paragraph.

Applicants argue that, "Accordingly, as Bjomson describes a method of analysis of segments that proceeds in parallel, rather than in serial, and as there is no suggestion in Bjornson et al. of the present method, Bjornson et al. fail to cure the deficiencies of the primary reference to Califano, including those acknowledged by the examiner to exist, so that the combination of Califano and Bjornson in rejection of the claims particularly as presently amended, is untenable. Therefore, withdrawal of this ground of rejection is believed to be in order, and is requested."

The Examiner respectfully disagrees. The citation that examiner used is from the "Background of the Invention," not the invention of Bjornson et al. Also, using a threshold on sequences query comparison can apply to both series or parallel comparison and will not affect the comparison process.

Claim Objections

3. **Claim 25** is objected because of the following informalities: Claim 25 recites "**dividing** each query sequence **into n+1 query sequence segments**..." and "for each query sequence, constructing a first query group and a second query group by placing individual query sequence segments in one of said query groups **such that at least n query sequence segments are contained in the second query group**..." which is not clear and leaves the examiner in doubt as to the meaning of the features to which they refer (e.g. Is "n" representing the range of "0 to infinity" or "1 to infinity"?). For example, if each query sequence is divided into n+1 segments, and at least n query sequence segments are contained in the second query group as cited above, then the first query group will contain 0 or 1 query sequence segment?

Clarification is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

a. Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

4. **Claims 55 are rejected under 35 U.S.C. § 101 because the claimed invention is directed to non-statutory subject matter.**

As to **claim 55,** it recites **"**removable computer-readable storage medium**"**, the specification does not clearly define which forms the above medium may take. Such a medium may take many forms, including, but not limited to, non-volatile, volatile and transmission media etc… If the computer readable medium may take the form of the transmission signal, this would render the claim not statutory because it's not tangible.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

5. **Claims 25, 31-34, 36, 38-41, 43-50, 52-54 and 56 rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson).**

For claim 25, Califano discloses a computer implemented method of searching biochemical data or information for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to n sequence positions, comprising:

a) dividing each query sequence into n+1 query sequence segments (Califano: column 5, lines 40-45, "the reference sequence is partitioned into substrings of contiguous tokens 35 at least two of which are non contiguously appended together 40 to form reference tuples.", where "segment" is read on "token") **and dividing each target fragment into at least n+1 target sequence fragment segments** (Califano: column 5, lines 32-35, "selecting an original string 10 from a database. The string is then partitioned into substrings of contiguous tokens 15 at least two of which are non contiguously appended together to form original tuples 20.");

b) for each query sequence, constructing a first query group and a second query group by placing individual query sequence segments in one of said query group such that at least n query sequence segments are contained in the second query group (Califano: column 5, lines 32-35, "the reference sequence is

partitioned into substrings of contiguous tokens 35 at least two of which are non contiguously appended together 40 to form reference tuples.");

c) for from each target sequence fragment segment, constructing a first target group according to the same distribution of segments as that of the first query group, and constructing a second target group according to the same distribution of segments as that of the second query group (Califano: column 5, lines 32-35, "selecting an original string 10 from a database. The string is then partitioned into substrings of contiguous tokens 15 at least two of which are non contiguously appended together to form original tuples 20.")**;**

d) for each query sequence, comparing the first query group with the corresponding first target group to identify a match (Califano: column 5, lines 46-47, "The reference indexes are then compared to the original indexes 50.")**.**

e) performing steps b). c) and d), for different distributions of segments (Califano: column 1, lines 35-40, "All tokens in the two sequences to be compared are considered pairwise to compute all possible candidate alignments between the two sequences.", column 8, lines 12-15, "Taking all possible ordered combinations of 3 contiguous and non contiguous substrings from this set of 17 substrings, it is possible to create 680 3 - tuples.")**; and**

f) for each match identified in steps d) and e), comparing the second query group with the second target group to identify a match, thereby identifying a query sequence in the set of target sequence fragments allowing for mismatches in up to n sequence positions (Colifano: column 2, lines 1-16, "The BLAST technique **does an in-depth comparison** of the original and reference sequence **only if they satisfy an initial minimal similarity test** which can be performed very quickly. This is done by heuristically determining whether the length of the MSP (maximal segment pair) is above **a given threshold.** The MSP is **the pair of identical length substrings of the reference string and sequence string that has the best score for mutations.** If this test is successful a more complete and costly similarity analysis is performed using FASTP-FASTA type algorithms. This reduces the amount of computation at risk of missing some matches that do not satisfy the initial criteria. About 20% of the similarities detected with the Needleman-Wunch algorithm are not picked up by BLAST. Also the approach remains inherently sequential since some computation must be performed for each token in the set of original strings." column 4, lines 55-63, "information in the EIT is used to locate token sequences on an original string in the database which correspond (exactly or similarly) to the reference sequence of tokens…", column 5, lines 32-35,

where "group" is read on “tuple”, and “tuples” indicates there are many group (e.g. first group, second group...etc.)).

However, Califano does not explicitly disclose discloses allowing for mismatches at up to n sequence positions.

Bjornson discloses allowing for mismatches at up to n sequence positions (Bjornson: column 2, lines 26-32, “first identify segments, with or without gaps, that are similar in a query sequence and a database sequence, then to evaluate the statistical significance of all such matches that are identified, and finally to summarize only those matches that satisfy a preselected threshold of significance.”, column 6, lines 14-32, “...such that the locally optimal ungapped alignment between the two members of said HSP achieves a score at least equal to a specified integer minimum score value or an e-score lower than a specified e-score threshold...”).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon “Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings” as taught by Califano by implementing “Method and apparatus for high-performance sequence comparison” as taught by Bjornson, because it would provide Califano’s method with

the enhanced capability of "`comparing sequences for similarity`" (Bjornson: column 6, lines 6-7).

For claim 31, Califano and Bjornson disclose the modified computer implemented method of claim 25, further comprising:

for each distinct distribution of query sequence segments, constructing a first query table indexed by possible values of the first query groups, wherein the entries in the first query table provide access to each second query group by using as an index the value of a corresponding first query group (Colifano: column 3, lines 21-29, "A large number of *indexes* are generated for each original string and are used to store a information record referring to the original string in a *look-up table*. During recognition, a large number of indexes are formed from a reference string. These are used to recover the information in the look-up table and to accumulate evidence for one or more original strings.").

For claim 32, Califano and Bjornson disclose the modified computer implemented method of claim 31, further comprising:

for each distinct distribution of query sequence segments, constructing a second query table providing access to each second query group, wherein the entries in the first query table provide references to appropriate entries in the second query table (Colifano: column 3, lines 21-29, lines 46-47, column 4, lines 27-63).

For claim 33, Califanoa and Bjornson disclose the modified computer implemented method of claim 31, further comprising:

for each first target group constructed in step (c), implementing step (d) by using each first target group to form an index into the first query table (Colifano: column 3, lines 21-29, lines 46-47).

For claim 34, Califano and Bjornson disclose the modified computer implemented method of claim 31, wherein, that the first query group of a first distribution is the same as the second query group of a second distribution, respective first query tables for each of the two distinct distributions are at least one of constructed and used concurrently (Colifano: column 3, lines 21-29, column 8, lines 12-15)

distributions of query sequence segments (Bjornson: column 4, 51-59)**.**

For claim 36, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein each query sequence of the plurality of query sequences and the target sequence fragments comprise nucleotide sequence data (Califano: column 1, lines 25-30, column 2, lines 62-67)**.**

For claim 38, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein n is at least two (Califano: column 6, lines 60-61)**.**

For claim 39, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein each query sequence of the plurality of query sequences and the target sequence fragments are divided into an even number of query sequence segments and target sequence fragment segments, and further wherein the query sequence segments and the target sequence

fragment segments are distributed in equal numbers between the first query group and the second query group and the first target group and a second target group (Bjornson: column 11, lines 7-10).

For claim 40, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein the n+1 query sequence segments are formed from a splitting of each query sequence of the plurality of query sequences (Califano: column 5, lines 32-35),

For claim 41, Califano and Bjornson discloses the modified computer implemented method of claim 25, wherein the n+1 query sequence segments are formed from a coding or scrambling of each query sequence of the plurality of query sequences (Califano: column 1, lines 35-40, column 8, lines 12-15).

For claim 43, Califano and Bjornson disclose the modified computer implemented method claim 25, further comprising: constructing or computing at least one hash function table (Califano: column 2, lines 52-55).

Claim 44 is rejected as substantially similar as claims 25, for the similar reasons.

Claim 45 is rejected as substantially similar as claims 27, for the similar reasons.

Claim 46 is rejected as substantially similar as claims 28, for the similar reasons.

Claim 47 is rejected as substantially similar as claims 31, for the similar reasons.

Claim 48 is rejected as substantially similar as claims 32, for the similar reasons.

Claim 49 is rejected as substantially similar as claims 40, for the similar reasons.

Claim 50 is rejected as substantially similar as claims 41, for the similar reasons.

Claim 52 is rejected as substantially similar as claims 43, for the similar reasons.

For claim 53, Califano and Bjornson disclose the modified apparatus of claim 44, wherein the apparatus is a personal computer or a desk top computer (Califano: column 5, lines 26-29)**.**

For claim 54, Califano discloses a computer program for installation and operation in a device for searching genetic data or information, said device for searching comprising a memory device, a processing device, a storage device and an output device, said computer program and comprising a computer program code for searching for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to n sequence positions, said computer program code comprising:

a first program module or portion for constructing in said memory device, for each query sequence of the plurality of query sequences (Califano: column 5, lines 26-29)**, a first query group and a second query group by dividing each query sequence of the plurality of query sequences into n+1 query sequence segments** (Califano: column 5, lines 32-45) **and distributing the query sequence segments between the first query group and the second query group in one or more ways such that at least n query sequence segments are contained in each second query group** (Califano: column 1, lines 35-40, column 5, lines 32-35)**;**

a second program module or portion for constructing in said memory device, for each target sequence fragment of the set of target sequence fragments, one or more first target groups having target sequence fragment

segment distributions corresponding to the first query groups (Califano: column 3, lines 21-29, column 4, lines 55-63, column 5, lines 32-35)**; and**

a third program module or portion for comparing, for each query sequence of the plurality of query sequences, one or more first query groups with corresponding one or more first target groups and to output a result identifying matching query sequences and matching target sequence fragments (Califano: column 4, lines 55-63, column 5, lines 46-47)**.**

However, Califano does not explicitly disclose discloses allowing for mismatches at up to n sequence positions.

Bjornson discloses allowing for mismatches at up to n sequence positions (Bjornson: column 2, lines 26-32, "first identify segments, with or without gaps, that are similar in a query sequence and a database sequence, then to evaluate the statistical significance of all such matches that are identified, and finally to summarize only those matches that satisfy a preselected threshold of significance.", column 6, lines 14-32, "...such that the locally optimal ungapped alignment between the two members of said HSP achieves a score at least equal to a specified integer minimum score value or an e-score lower than a specified e-score threshold...").

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token

sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Method and apparatus for high-performance sequence comparison" as taught by Bjornson, because it would provide Califano's program with the enhanced capability of "comparing sequences for similarity " (Bjornson: column 6, lines 6-7).

For claim 56, Califano and Bjornson disclose the modified computer program of claim 54, wherein the computer program is loadable on a device for searching, over a network connection. 9 (Bojornson: column 5, lines 49-65).

6. **Claims 29, 30 and 37 are rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson) as applied in claim 25 above, and further in view of Patzer (U.S. Patent No.: US 2004/0059721 A1).**

For claim 29, Califano and Bjornson disclose the modified computer implemented method of claim 25.

However, Califano and Bjornson do not explicitly disclose wherein step (f) is carried out by applying an exclusive OR operation to a binary representation of each of the second query group and the second target group.

Patzer discloses wherein step (f) is carried out by applying an exclusive OR operation to a binary representation of each of the second query group and the

second target group (Patzer: page 1, paragraph [0012], "Using this encoding, the system adds the result of every *XOR* nucleotide comparison")**.**

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Method and apparatus for high-performance sequence comparison" as taught by Patzer, because it would provide Califano and Bjornson's modified method with the enhanced capability of "in order to obtain a sum score quantifying the dissimilarity of a particular sequence alignment." (Patzer: page 1, paragraph [0012]).

For claim 30, Califano, Bjornson and Patzer disclose the modified computer implemented method of claim 29, wherein a result is analyzed using a lookup table (Califano: column 1, lines 45-59, "...are matched for both sequences using a look-up table that is created from the reference string. The score for each candidate match is computed and the best score is selected...")**.**

the exclusive OR operation (Patzer: page 1, paragraph [0012]).

For claim 37, Califano and Bjornson disclose the modified computer implemented method of claim 36.

However, Califano and Bjornson do not explicitly disclose wherein each query sequence of the plurality of query sequences and the target sequence fragments are binary encoded.

Patzer discloses wherein each query sequence of the plurality of query sequences and the target sequence fragments are binary encoded (Patzer: page 5, paragraph [0096])**.**

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Method and apparatus for high-performance sequence comparison" as taught by Patzer, because it would provide Califano and Bjornson's modified method with the enhanced capability of "in order to obtain a sum

score quantifying the dissimilarity of a particular sequence alignment." (Patzer: page 1, paragraph [0012]).

7. **Claims 35 and 55 are rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson) as applied in claims 25 and 54 above, and further in view of Walker et al. (U.S. Patent No.: US 6,633,817 B1, hereinafter, Walker).**

For claim 35, Califano and Bjornson disclose the modified computer implemented method of claim 25.

However Califano and Bjornson do not explicitly disclose wherein target sequence fragments in the set of target sequence fragments comprise overlapping fragments of one or more target sequences.

Walker discloses wherein target sequence fragments in the set of target sequence fragments comprise overlapping fragments of one or more target sequences (Walker: column 1, lines 61-65, "partitioned into a plurality of overlapping windows or fragments…")**.**

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Sequence database search with sequence search trees"

as taught by Walker, because it would provide Califano and Bjornson's modified method with the enhanced capability of "organizing and searching database sequences that is fast and efficient, and at the same time provides a high degree of accuracy, that is, one that identifies sequences similar to a query sequence." (Walker: column 1, lines 46-50).

For claim 55, Califano and Bjornson disclose the modified computer program of claim 54.

However, Califano and Bjornson do not explicitly disclsoe wherein the computer program is stored on a removable computer-readable storage medium.

Walker discloses the computer program of claim 54, wherein the computer program is stored on a removable computer-readable storage medium (Walker: claim 22).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Sequence database search with sequence search trees" as taught by Walker, because it would provide Califano and Bjornson's modified program with the enhanced capability of storing and executing a program by computers.

8. **Claims 42 and 51 are rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in**

view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson) as applied in claims 25 and 54 above, and further in view of Myers et al. (U.S. Patent No.: US 6,714,874 B1, hereinafter, Myers).

For claim 42, Califano and Bjornson discloses the modified computer implemented method of claim 25, further comprising: using a hash function to split each query sequence of the plurality of query sequences and the target sequence fragments (Califano: column 2, lines 52-55)**.**

However, Califano and Bjornson do not explicitly disclose further comprising: using a hash function to split each query sequence of the plurality of query sequences and the target sequence fragments into prefixes and suffixes.

Myers discloses further comprising: using a hash function to split each query sequence of the plurality of query sequences and the target sequence fragments into prefixes and suffixes (Myers: column 9, lines 52-53, column 13, 52-61)**.**

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Method and system for the assembly of a whole genome using a shot-gun data set" as taught by Myers, because it would provide Califano and Bjornson's modified method with the enhanced capability of "A containment relationship between fragment-ends is a further

refinement of a containment relationship between fragments."

(Myers: column 13, lines 50-52).

Claim 51 is rejected as substantially similar as claims 42, for the similar reasons.

9. **Claim 57 is rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson) as applied in claim 25 above, and further in view of Harris et al. (U.S. Pub. No.: US 2002/0022243 A1, hereinafter, Harris).**

For claim 57, Califano and Bjornson disclose the modified computer implemented method of claim 25.

However, Califano and Bjornson does not explicitly disclose, wherein each query sequence of the plurality of query sequences and the target sequence fragments comprise polypeptide sequence data.

Harris discloses wherein each query sequence of the plurality of query sequences and the target sequence fragments comprise polypeptide sequence data. (Harris: page 11, paragraph [0141]).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Profiling of protease specificity using

combinatorial fluorogenic substrate libraries" as taught by Harris, because it would provide Califano and Bjornson's modified method with the enhanced capability of "provides a computer system for comparing a query polypeptide sequence or query peptide sequence specificity to a database containing an array of data structures..." (Harris: page 11, paragraph [0141]).

Conclusion

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to YU ZHAO whose telephone number is (571)270-3427. The examiner can normally be reached on Monday-Friday 7:30am-5:00pm EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Mahmoudi, Tony can be reached on (571) 272-4078. The fax phone number for the organization where this application or proceeding is assigned is 571-270-4427.

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Date: 7/15/2009

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Examiner, Art Unit 2169

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